

This page gives you Search Results detail for the Application 10650507 and Search Result us-10-650-507-8.rag.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:09:29 ; Search time 200 Seconds  
(without alignments)  
1483.667 Million cell updates/sec

Title: US-10-650-507-8  
Perfect score: 3518  
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3518	100.0	649	2	AAY14541	Aay14541 Human lip
2	3518	100.0	649	3	AAY95822	Aay95822 Human lip
3	3518	100.0	649	4	AAB59901	Aab59901 Human lep
4	3507.5	99.7	650	8	ADP46576	Adp46576 Human col
5	3401.5	96.7	630	2	AAY14542	Aay14542 Human lip
6	3401.5	96.7	630	3	AAY95823	Aay95823 Human lip

7	3401.5	96.7	630	4	AAB59902	Aab59902	Human lep
8	3372.5	95.9	630	8	ADR08703	Adr08703	Human pro
9	3169	90.1	591	5	ABP68616	Abp68616	Human pan
10	3169	90.1	591	9	ADY15926	Ady15926	PRO polyp
11	3169	90.1	591	9	ADY20195	Ady20195	PRO polyp
12	3121	88.7	583	4	AAB88476	Aab88476	Human mem
13	3121	88.7	583	9	ADY63313	Ady63313	Human clo
14	3058	86.9	581	2	AAAY14543	Aay14543	Human lip
15	3058	86.9	581	3	AAAY95824	Aay95824	Human lip
16	3058	86.9	581	4	AAB59903	Aab59903	Human lep
17	2568	73.0	593	2	AAAY14538	Aay14538	Rat lipol
18	2568	73.0	593	4	AAB59904	Aab59904	Rat lepti
19	2519.5	71.6	594	2	AAAY14544	Aay14544	Mouse lip
20	2519.5	71.6	594	4	AAB59907	Aab59907	Murine le
21	2474.5	70.3	574	2	AAAY14539	Aay14539	Rat lipol
22	2474.5	70.3	574	4	AAB59905	Aab59905	Rat lepti
23	2426	69.0	575	2	AAAY14545	Aay14545	Mouse lip
24	2426	69.0	575	4	AAB59908	Aab59908	Murine le
25	2142	60.9	525	2	AAAY14540	Aay14540	Rat lipol
26	2142	60.9	525	4	AAB59906	Aab59906	Rat lepti
27	2095.5	59.6	526	2	AAAY14546	Aay14546	Mouse lip
28	2095.5	59.6	526	4	AAB59909	Aab59909	Murine le
29	1827.5	51.9	388	8	ADP46577	Adp46577	Human col
30	1138	32.3	208	8	ABO59373	Abo59373	Human gen
31	823.5	23.4	163	3	AAB53495	Aab53495	Human col
32	726	20.6	227	8	ADP46526	Adp46526	Human col
33	642.5	18.3	546	6	ABR43174	Abr43174	Human REM
34	638.5	18.1	540	8	ADR89882	Adr89882	FREP poly
35	637.5	18.1	635	8	ADR89880	Adr89880	FREP poly
36	502.5	14.3	265	7	ADM56943	Adm56943	Human cyt
37	465.5	13.2	241	7	ADM56944	Adm56944	Mature hu
38	452	12.8	428	4	AAU18010	Aau18010	Human imm
39	452	12.8	428	7	ADB31634	Adb31634	Human nov
40	452	12.8	430	4	ABB10256	Abb10256	Human cDN
41	452	12.8	430	5	ABP66843	Abp66843	Human pol
42	349	9.9	204	4	AAU18069	Aau18069	Human imm
43	349	9.9	204	4	ABB10461	Abb10461	Human cDN
44	349	9.9	204	5	ABP67048	Abp67048	Human pol
45	349	9.9	204	7	ADB31693	Adb31693	Human nov

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:18:25 ; Search time 51 Seconds  
(without alignments)  
1113.870 Million cell updates/sec

Title: US-10-650-507-8  
Perfect score: 3518  
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	3518	100.0	649	2	US-09-499-522-14	Sequence 14, Appl
2	3518	100.0	649	2	US-09-269-939A-8	Sequence 8, Appli
3	3401.5	96.7	630	2	US-09-499-522-16	Sequence 16, Appl
4	3401.5	96.7	630	2	US-09-269-939A-10	Sequence 10, Appl
5	3058	86.9	581	2	US-09-499-522-18	Sequence 18, Appl
6	3058	86.9	581	2	US-09-269-939A-12	Sequence 12, Appl
7	2568	73.0	593	2	US-09-269-939A-2	Sequence 2, Appli
8	2519.5	71.6	594	2	US-09-269-939A-16	Sequence 16, Appl

9	2474.5	70.3	574	2	US-09-269-939A-4	Sequence 4, Appli
10	2426	69.0	575	2	US-09-269-939A-17	Sequence 17, Appl
11	2142	60.9	525	2	US-09-269-939A-6	Sequence 6, Appli
12	2095.5	59.6	526	2	US-09-269-939A-18	Sequence 18, Appl
13	169.5	4.8	715	2	US-10-104-047-3385	Sequence 3385, Ap
14	166	4.7	977	2	US-09-252-991A-16655	Sequence 16655, A
15	153.5	4.4	437	2	US-09-538-092-876	Sequence 876, App
16	153.5	4.4	614	5	PCT-US95-03236-21	Sequence 21, Appl
17	153	4.3	316	2	US-09-397-243D-13	Sequence 13, Appl
18	150	4.3	767	2	US-09-252-991A-28262	Sequence 28262, A
19	150	4.3	1382	2	US-09-171-991-9	Sequence 9, Appli
20	150	4.3	1388	2	US-09-949-016-10817	Sequence 10817, A
21	148	4.2	1462	2	US-09-538-092-1043	Sequence 1043, Ap
22	148	4.2	1462	2	US-09-949-002-381	Sequence 381, App
23	148	4.2	1524	2	US-09-949-002-495	Sequence 495, App
24	146.5	4.2	777	2	US-09-252-991A-27864	Sequence 27864, A
25	146	4.2	998	2	US-09-949-016-7757	Sequence 7757, Ap
26	145.5	4.1	319	1	US-08-597-495B-22	Sequence 22, Appl
27	145.5	4.1	319	2	US-09-068-051A-22	Sequence 22, Appl
28	145.5	4.1	319	2	US-09-336-536-67	Sequence 67, Appl
29	145.5	4.1	319	2	US-09-254-465A-6	Sequence 6, Appli
30	145.5	4.1	319	2	US-09-953-499-6	Sequence 6, Appli
31	145.5	4.1	757	2	US-10-094-749-2685	Sequence 2685, Ap
32	144.5	4.1	691	2	US-09-252-991A-16809	Sequence 16809, A
33	144.5	4.1	783	2	US-09-252-991A-18035	Sequence 18035, A
34	143	4.1	636	2	US-09-252-991A-24902	Sequence 24902, A
35	143	4.1	743	2	US-09-902-540-10164	Sequence 10164, A
36	142.5	4.1	264	2	US-09-252-991A-20342	Sequence 20342, A
37	142	4.0	399	2	US-09-252-991A-25039	Sequence 25039, A
38	141.5	4.0	387	2	US-09-252-991A-30467	Sequence 30467, A
39	141	4.0	302	1	US-08-893-853-3	Sequence 3, Appli
40	141	4.0	302	2	US-09-113-921-3	Sequence 3, Appli
41	141	4.0	302	2	US-09-451-067-3	Sequence 3, Appli
42	141	4.0	302	3	US-10-086-208-3	Sequence 3, Appli
43	140	4.0	560	2	US-09-252-991A-26107	Sequence 26107, A
44	139.5	4.0	424	2	US-09-252-991A-22384	Sequence 22384, A
45	139	4.0	412	2	US-09-252-991A-23193	Sequence 23193, A

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:19:15 ; Search time 182 Seconds  
(without alignments)  
1651.794 Million cell updates/sec

Title: US-10-650-507-8  
Perfect score: 3518  
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	3518	100.0		649	4	US-10-214-684A-14	Sequence 14, Appl
2	3518	100.0		649	4	US-10-650-507-8	Sequence 8, Appli
3	3518	100.0		649	6	US-11-236-198-3	Sequence 3, Appli
4	3401.5	96.7		630	4	US-10-214-684A-16	Sequence 16, Appl
5	3401.5	96.7		630	4	US-10-650-507-10	Sequence 10, Appl
6	3401.5	96.7		630	6	US-11-236-198-5	Sequence 5, Appli
7	3251	92.4		601	5	US-10-756-149-5066	Sequence 5066, Ap
8	3169	90.1		591	4	US-10-060-036-165	Sequence 165, App
9	3058	86.9		581	4	US-10-214-684A-18	Sequence 18, Appl
10	3058	86.9		581	4	US-10-650-507-12	Sequence 12, Appl

11	3058	86.9	581	6	US-11-236-198-7	Sequence 7, Appli
12	2568	73.0	593	4	US-10-650-507-2	Sequence 2, Appli
13	2568	73.0	593	6	US-11-236-198-9	Sequence 9, Appli
14	2519.5	71.6	594	4	US-10-650-507-16	Sequence 16, Appl
15	2519.5	71.6	594	6	US-11-236-198-17	Sequence 17, Appl
16	2474.5	70.3	574	4	US-10-650-507-4	Sequence 4, Appli
17	2474.5	70.3	574	6	US-11-236-198-11	Sequence 11, Appl
18	2426	69.0	575	4	US-10-650-507-17	Sequence 17, Appl
19	2426	69.0	575	6	US-11-236-198-18	Sequence 18, Appl
20	2142	60.9	525	4	US-10-650-507-6	Sequence 6, Appli
21	2142	60.9	525	6	US-11-236-198-13	Sequence 13, Appl
22	2095.5	59.6	526	4	US-10-650-507-18	Sequence 18, Appl
23	2095.5	59.6	526	6	US-11-236-198-19	Sequence 19, Appl
24	1138	32.3	208	4	US-10-029-386-33007	Sequence 33007, A
25	823.5	23.4	163	3	US-09-925-299-1035	Sequence 1035, Ap
26	823.5	23.4	163	3	US-09-925-299-1035	Sequence 1035, Ap
27	452	12.8	428	4	US-10-091-438-155	Sequence 155, App
28	452	12.8	430	3	US-09-764-853-564	Sequence 564, App
29	349	9.9	204	3	US-09-764-853-769	Sequence 769, App
30	349	9.9	204	4	US-10-091-438-214	Sequence 214, App
31	325	9.2	175	4	US-10-264-237-2542	Sequence 2542, Ap
32	251.5	7.1	138	4	US-10-029-386-29424	Sequence 29424, A
33	249.5	7.1	124	3	US-09-864-761-48029	Sequence 48029, A
34	233.5	6.6	110	3	US-09-864-761-37731	Sequence 37731, A
35	185	5.3	2263	4	US-10-408-765A-2231	Sequence 2231, Ap
36	185	5.3	2296	5	US-10-696-909A-46	Sequence 46, Appl
37	185	5.3	2752	5	US-10-696-909A-44	Sequence 44, Appl
38	169.5	4.8	715	4	US-10-104-047-3385	Sequence 3385, Ap
39	169.5	4.8	715	6	US-11-072-512-3385	Sequence 3385, Ap
40	166	4.7	448	6	US-11-097-143-8784	Sequence 8784, Ap
41	166	4.7	19652	4	US-10-084-846A-7	Sequence 7, Appli
42	163	4.6	1231	6	US-11-097-143-6006	Sequence 6006, Ap
43	162.5	4.6	505	4	US-10-264-049-3123	Sequence 3123, Ap
44	162	4.6	272	4	US-10-767-701-41627	Sequence 41627, A
45	161.5	4.6	1243	5	US-10-450-763-51580	Sequence 51580, A

This page gives you Search Results detail for the Application 10650507 and Search Result \$itemName.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:20:10 ; Search time 16 Seconds  
(without alignments)  
512.840 Million cell updates/sec

Title: US-10-650-507-8  
Perfect score: 3518  
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	152.5	4.3		655	7	US-11-293-697-2723	Sequence 2723, Ap
2	148	4.2		374	6	US-10-953-349-33957	Sequence 33957, A
3	146.5	4.2		347	6	US-10-953-349-3425	Sequence 3425, Ap
4	136	3.9		407	6	US-10-953-349-24955	Sequence 24955, A
5	136	3.9		471	6	US-10-953-349-24954	Sequence 24954, A
6	136	3.9		482	6	US-10-953-349-24953	Sequence 24953, A
7	133.5	3.8		523	6	US-10-953-349-35575	Sequence 35575, A
8	133	3.8		318	6	US-10-953-349-27945	Sequence 27945, A



9	133	3.8	343	6	US-10-953-349-27944	Sequence 27944, A
10	133	3.8	394	6	US-10-953-349-27943	Sequence 27943, A
11	132.5	3.8	377	6	US-10-953-349-35827	Sequence 35827, A
12	132	3.8	288	6	US-10-953-349-17941	Sequence 17941, A
13	132	3.8	834	6	US-10-953-349-9789	Sequence 9789, Ap
14	132	3.8	854	6	US-10-953-349-9788	Sequence 9788, Ap
15	132	3.8	878	6	US-10-953-349-9787	Sequence 9787, Ap
16	128.5	3.7	448	7	US-11-293-697-4755	Sequence 4755, Ap
17	127.5	3.6	353	6	US-10-953-349-35828	Sequence 35828, A
18	127.5	3.6	1460	7	US-11-247-437-14	Sequence 14, Appl
19	127	3.6	322	6	US-10-953-349-21883	Sequence 21883, A
20	125.5	3.6	382	6	US-10-953-349-2030	Sequence 2030, Ap
21	124.5	3.5	1935	6	US-10-480-962-6	Sequence 6, Appli
22	123.5	3.5	303	6	US-10-953-349-5570	Sequence 5570, Ap
23	123	3.5	671	6	US-10-196-749-346	Sequence 346, App
24	122.5	3.5	303	6	US-10-953-349-266	Sequence 266, App
25	121	3.4	596	6	US-10-953-349-35610	Sequence 35610, A
26	120	3.4	352	6	US-10-953-349-2031	Sequence 2031, Ap
27	118.5	3.4	542	7	US-11-293-697-4713	Sequence 4713, Ap
28	118	3.4	261	6	US-10-953-349-35829	Sequence 35829, A
29	117.5	3.3	363	6	US-10-953-349-24729	Sequence 24729, A
30	117.5	3.3	400	6	US-10-953-349-24728	Sequence 24728, A
31	117.5	3.3	583	6	US-10-953-349-35611	Sequence 35611, A
32	117	3.3	422	6	US-10-953-349-24756	Sequence 24756, A
33	117	3.3	458	6	US-10-953-349-24755	Sequence 24755, A
34	117	3.3	1023	7	US-11-293-697-3123	Sequence 3123, Ap
35	116	3.3	286	6	US-10-953-349-24757	Sequence 24757, A
36	115	3.3	390	6	US-10-953-349-22063	Sequence 22063, A
37	114.5	3.3	611	7	US-11-321-421-81	Sequence 81, Appl
38	114	3.2	310	6	US-10-953-349-12367	Sequence 12367, A
39	114	3.2	632	7	US-11-293-697-3548	Sequence 3548, Ap
40	113	3.2	621	7	US-11-293-697-3069	Sequence 3069, Ap
41	112.5	3.2	333	6	US-10-953-349-24730	Sequence 24730, A
42	112.5	3.2	373	6	US-10-953-349-31149	Sequence 31149, A
43	112.5	3.2	1126	7	US-11-293-697-3665	Sequence 3665, Ap
44	112	3.2	949	7	US-11-293-697-3033	Sequence 3033, Ap
45	111	3.2	237	6	US-10-953-349-27001	Sequence 27001, A



This page gives you Search Results detail for the Application 10650507 and Search Result us-10-650-507-8.rpr.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:13:19 ; Search time 44 Seconds  
(without alignments)  
1419.197 Million cell updates/sec

Title: US-10-650-507-8  
Perfect score: 3518  
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	170	4.8	1173	2	T31421	C-terminal domain-	
2	166	4.7	448	2	A36311	70K U1 small nucle	
3	153.5	4.4	614	2	A25707	U1 snRNP 70K prote	
4	149.5	4.2	1344	2	T42637	hypothetical prote	
5	148	4.2	1403	1	A47328	natural killer cel	
6	146.5	4.2	347	2	T08954	hypothetical prote	
7	145	4.1	3942	2	T42730	Bassoon protein -	
8	144.5	4.1	378	2	S04336	U1 snRNP 70K prote	
9	144.5	4.1	670	2	T49510	fibroin-3 related	
10	144.5	4.1	3938	2	T42761	Bassoon protein -	
11	143.5	4.1	998	2	T30930	hypothetical prote	
12	143.5	4.1	2022	2	T48818	glucan 1,4-alpha-g	

13	143	4.1	2212	2	A41098	calcium channel pr
14	142.5	4.1	834	2	T42702	hypothetical prote
15	142	4.0	632	2	T02627	hypothetical prote
16	142	4.0	1208	2	T23467	hypothetical prote
17	141.5	4.0	948	2	A57640	retinoblastoma bin
18	141.5	4.0	963	2	T19140	hypothetical prote
19	141	4.0	2649	2	T51023	hypothetical prote
20	140.5	4.0	604	2	T37994	probable splicing
21	140	4.0	344	2	S59043	splicing factor SR
22	139.5	4.0	370	2	A87358	hypothetical prote
23	139.5	4.0	618	2	T42664	hypothetical prote
24	139	4.0	1571	2	T00062	hypothetical prote
25	138.5	3.9	335	2	T21503	hypothetical prote
26	138.5	3.9	489	2	A45988	dentin matrix acid
27	138	3.9	1888	2	S78476	collagen alpha 1(X
28	136	3.9	3124	2	A40020	collagen alpha 1(X
29	135	3.8	1870	2	S37671	MHC class III hist
30	134	3.8	309	2	T47685	probable RNA bindi
31	134	3.8	1097	2	T13033	cyclin T - fruit f
32	133.5	3.8	771	2	T21633	hypothetical prote
33	133.5	3.8	868	2	JC5701	ErbB kinase activa
34	133.5	3.8	2142	2	B35098	MHC class III hist
35	133	3.8	375	2	A40112	MHC-region RD-repe
36	132.5	3.8	287	2	T50647	serine/arginine-ri
37	132.5	3.8	374	2	A37282	52K active chromat
38	132.5	3.8	825	1	EDBEXD	immediate-early pr
39	132.5	3.8	1520	2	T00273	hypothetical prote
40	132.5	3.8	2774	2	A43359	microtubule-associ
41	132	3.8	309	2	A39773	myristylated alani
42	132	3.8	562	2	T26242	hypothetical prote
43	132	3.8	611	1	S12566	translation initia
44	132	3.8	725	2	T00492	hypothetical prote
45	131.5	3.7	697	2	JC2365	fused proteinase-c

This page gives you Search Results detail for the Application 10650507 and Search Result us-10-650-507-8.rup.  
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:09:44 ; Search time 303 Seconds  
(without alignments)  
1981.304 Million cell updates/sec

Title: US-10-650-507-8  
Perfect score: 3518  
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	3518	100.0	649	2	Q86X29_HUMAN	Q86x29 homo sapien		
2	3372.5	95.9	630	2	Q6ZT80_HUMAN	Q6zt80 homo sapien		
3	3169	90.1	591	2	Q9UQL3_HUMAN	Q9uql3 homo sapien		
4	3124	88.8	583	2	Q9BT33_HUMAN	Q9bt33 homo sapien		
5	3121	88.7	583	2	Q8NBM0_HUMAN	Q8nbm0 homo sapien		
6	3116	88.6	582	2	Q9BWS2_HUMAN	Q9bws2 homo sapien		
7	2619.5	74.5	656	2	Q61148_MOUSE	Q61148 mus musculu		
8	2568	73.0	593	2	Q9WU74_RAT	Q9wu74 rattus norv		
9	2526.5	71.8	594	2	Q99KG5_MOUSE	Q99kg5 mus musculu		
10	2474.5	70.3	574	2	Q9WU75_RAT	Q9wu75 rattus norv		
11	2470.5	70.2	574	2	Q497B9_RAT	Q497b9 rattus norv		
12	2446.5	69.5	576	2	Q6U816_MOUSE	Q6u816 mus musculu		
13	2433	69.2	575	2	Q3UIQ9_MOUSE	Q3uiq9 mus musculu		
14	2304	65.5	429	2	O00112_HUMAN	O00112 homo sapien		

15	2142	60.9	525	2	Q9WU76_RAT	Q9wu76	rattus norv
16	2093.5	59.5	526	2	Q3TJE7_MOUSE	Q3tje7	mus musculu
17	1554.5	44.2	575	2	Q6GPK3_XENLA	Q6gpk3	xenopus lae
18	1460.5	41.5	270	2	O00426_HUMAN	O00426	homo sapien
19	1340	38.1	248	2	Q499Z8_HUMAN	Q499z8	homo sapien
20	1331	37.8	339	2	Q61149_MOUSE	Q61149	mus musculu
21	1174.5	33.4	638	2	Q6GMG1_BRARE	Q6gmg1	brachydanio
22	1159	32.9	594	2	Q4V8Y3_BRARE	Q4v8y3	brachydanio
23	965	27.4	639	2	Q71H61_HUMAN	Q71h61	homo sapien
24	722.5	20.5	663	2	Q4SHQ6_TETNG	Q4shq6	tetraodon n
25	715.5	20.3	557	2	Q4KMJ6_BRARE	Q4kmj6	brachydanio
26	676.5	19.2	194	2	Q4T5P9_TETNG	Q4t5p9	tetraodon n
27	634.5	18.0	546	2	Q5R8C7_PONPY	Q5r8c7	pongo pygma
28	616.5	17.5	502	2	Q86SU0_HUMAN	Q86su0	homo sapien
29	608.5	17.3	537	2	Q8CBR1_MOUSE	Q8cbr1	mus musculu
30	607.5	17.3	545	2	Q32NM7_XENLA	Q32nm7	xenopus lae
31	598.5	17.0	516	2	Q91VS0_MOUSE	Q91vs0	mus musculu
32	595.5	16.9	493	2	Q6PFB3_MOUSE	Q6pfb3	mus musculu
33	595.5	16.9	516	2	Q8CB39_MOUSE	Q8cb39	mus musculu
34	556.5	15.8	550	2	Q66L52_BRARE	Q66l52	brachydanio
35	548	15.6	573	2	Q4S0L1_TETNG	Q4s0l1	tetraodon n
36	547.5	15.6	464	2	Q7T2Z9_BRARE	Q7t2z9	brachydanio
37	545	15.5	470	2	Q4SHT3_TETNG	Q4sht3	tetraodon n
38	506	14.4	559	2	Q4S0L2_TETNG	Q4s0l2	tetraodon n
39	502.5	14.3	265	2	Q7Z578_HUMAN	Q7z578	homo sapien
40	190.5	5.4	96	2	Q4T5Q0_TETNG	Q4t5q0	tetraodon n
41	188	5.3	836	2	Q4WU48_ASPFU	Q4wu48	aspergillus
42	185	5.3	956	2	Q9UQ39_HUMAN	Q9uq39	homo sapien
43	185	5.3	1022	2	Q6NSL3_HUMAN	Q6nsl3	homo sapien
44	185	5.3	1262	2	Q9UQ40_HUMAN	Q9uq40	homo sapien
45	185	5.3	2296	2	Q9UHA8_HUMAN	Q9uha8	homo sapien